

SEQUENCE LISTING

<110> Xia, Zhi-Qiang  
Costa, Michael A  
Davin, Laurence B  
Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and  
methods of Use

<130> wsurl13787

<140> Not yet assigned  
<141> 1999-04-23

<150> 60/082, 977  
<151> 1998-04-24

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<170> PatentIn Ver. 2.0

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ctt ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc 96  
 Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu  
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ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144  
 Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu  
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atc cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240  
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
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aac aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca 285
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala
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atg aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile 130	135	140	432
att tcc act gct agt tta agc tca act atg ggt ggt tct tca cat Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His 145	150	155	480
gcc tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu 165	170	175	528
gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro 180	185	190	576
ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat Phe Gly Leu Pro Thr Ala Leu Gly Lys Phe Ser Gly Ile Lys Asn 195	200	205	624
gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly 210	215	220	672
cca aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Leu Tyr Leu Ala 225	230	235	720
agt gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly 245	250	255	768
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Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr  
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Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
 65 70 75 80

Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala  
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Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala  
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Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys  
 115 120 125

Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile  
 130 135 140

Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His  
 145 150 155 160

Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu  
 165 170 175

Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro  
 180 185 190

Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn  
 195 200 205

Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly  
 210 215 220

Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala  
 225 230 235 240

Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly  
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Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr  
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aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat 144  
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp  
35 40 45

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Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser  
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ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac 336  
Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp  
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aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga 384  
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly  
115 120 125

gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc 432  
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg  
130 135 140

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145 150 155 160

ggt tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt 528  
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu  
165 170 175

act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat 576  
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn  
180 185 190

tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca 624  
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser  
195 200 205

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Gly Ile Lys Asn Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly  
210 215 220

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															255
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Thr	Ala	Lys	Leu	Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp
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Val	Gln	Asp	Glu	Leu	Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser
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Phe	Ser	Asn	Ala	Gly	Ile	Ser	Asp	Pro	Asn	Arg	Pro	Arg	Ile	Ile	Asp
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Asn	Glu	Lys	Ala	Asp	Phe	Glu	Arg	Val	Phe	Ser	Val	Asn	Val	Thr	Gly
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Val	Phe	Leu	Cys	Met	Lys	His	Ala	Ala	Arg	Val	Met	Ile	Pro	Ala	Arg
						130			135						140
Ser	Gly	Asn	Ile	Ile	Ser	Thr	Ala	Ser	Leu	Ser	Ser	Thr	Met	Gly	Gly
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Gly	Ser	Ser	His	Ala	Tyr	Cys	Gly	Ser	Lys	His	Ala	Val	Leu	Gly	Leu
						165			170						175
Thr	Arg	Asn	Leu	Ala	Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn
						180			185						190

Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser  
 195 200 205  
 Gly Ile Lys Asn Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly  
 210 215 220  
 Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala  
 225 230 235 240  
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu  
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 Gln Tyr Pro Asp Ser  
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 ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca gca aaa ctc 96  
 Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu  
 20 25 30  
 ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144  
 Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu  
 35 40 45  
 tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac 192  
 Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr  
 50 55 60  
 atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240  
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
 65 70 75 80  
 aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca 288  
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala  
 85 90 95  
 gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca 336  
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala  
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Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His			
145	150	155	160
gct tat tgt gca aaa cat gct gta tta ggc ctt act agg aat ctg		528	
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu			
165	170	175	
gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct		576	
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro			
180	185	190	
ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat		624	
Phe Gly Leu Pro Thr Pro Leu Ala Lys Phe Ser Gly Ile Glu Asn			
195	200	205	
gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt		672	
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly			
210	215	220	
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Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala			
225	230	235	240
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Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly			
245	250	255	
ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac		816	
Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp			
260	265	270	
tct		819	
Ser			

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&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Forsythia x intermedia

&lt;400&gt; 6

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5

10

15

Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu

20

25

30

Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu

35

40

45

Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr  
 50 55 60  
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
 65 70 75 80  
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala  
 85 90 95  
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala  
 100 105 110  
 Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe  
 115 120 125  
 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile  
 130 135 140  
 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His  
 145 150 155 160  
 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu  
 165 170 175  
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro  
 180 185 190  
 Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn  
 195 200 205  
 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly  
 210 215 220  
 Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala  
 225 230 235 240  
 Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly  
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Ser

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Leu	Ile	Thr	gga	
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gtt	gcc	aaa	gtt	
Gly	Ala	Gly	Ala	
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Asn	Val	Ser	Ile	
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Ala	Ile	Ala	Asp	
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gtc	caa	gat	gaa	192
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Gly	Leu	Gly	His	
gtt	gtc	gag	tca	
Ala	Ile	Gly	Val	
act	gcc	atc	gac	
Asp	Asn	Tyr	His	
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gac	atc	atc	gat	
Asn	Ser	Ile	Tyr	
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aat	tcc	atc	acc	240
Asn	Ser	Ile	Tyr	
gat	acc	acc	aat	
Asp	Asn	His	Cys	
85	90	95		
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Asn	Ala	Asp	Asn	
gac	aac	aca	gtt	
Val	Asn	Thr	Val	
acc	tca	acc	tat	
Thr	Val	Ser	His	
gga	aaa	ctg	gac	
Asp	Val	Tyr	Asp	
95	100	105	110	
att	gct	gac	att	
Asn	Asn	Gly	Ile	
100	105	110		
gac	ccc	acc	ccc	336
Phe	Asn	Ala	Asp	
105	110			
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Asn	Glu	Asp	Phe	
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Asn	Glu	Arg	Gly	
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Val	Phe	Leu	Cys	
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Phe	Leu	Cys	Met	
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Ile	Ile	tat	tgt	
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Thr	Arg	Asn	Leu	
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Cys	Leu	Ala	Pro	
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Asn	Leu	Ala	Tyr	
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gca	gca	gtt	atg	
Ala	Ala	Leu	Ala	
185	190	195	200	
gtt	tcc	gtt	atg	672
Gly	Leu	Glu	Asn	
190	195	200	205	
atc	gca	act	gtc	
Asn	Leu	Ser	Asp	
195	200	205		
gca	gca	gtt	atg	
Ala	Ala	Leu	Gly	
200	205	210	215	
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Asn	Leu	Gly	Thr	
205	210	215	220	
atc	gca	act	gtc	
Asn	Leu	Ser	Asp	
210	215	220	225	
gca	gca	gtt	atg	
Ala	Ala	Leu	Gly	
215	220	225	230	
gtt	tcc	gtt	atg	
Asn	Leu	Gly	Thr	
220	225	230	235	
atc	gca	act	gtc	
Asn	Leu	Ser	Asp	
225	230	235	240	

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ctt tat ctg gca agt gat gag gca aaa tat gtg agt gga cac aat ctg	768		
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu			
245	255		
ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc	816		
Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe			
260	265	270	
caa tat cca gac act	831		
Gln Tyr Pro Asp Thr			
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Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met			
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Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp			
100	105	110	
Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly			
115	120	125	
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg			
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Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly			
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Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu			
165	170	175	
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn			
180	185	190	
Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val			
195	200	205	

Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly  
 210 215 220  
 Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala  
 225 230 235 240  
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu  
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 Lys Val Ala Leu Ile Thr Gly Ala Ser Gly Val Gly Glu Val Thr  
 20 25 30  
 gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc 144  
 Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val  
 35 40 45  
 caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat 192  
 Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn  
 50 55 60  
 tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat 240  
 Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn  
 65 70 75 80  
 gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc 288  
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe  
 85 90 95  
 aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac 336  
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn  
 100 105 110  
 gaa aaa gca gac ttt gaa cgc gtt ctc agt gtt aat gta acc gga gtt 384  
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val  
 115 120 125

ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt	432
Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser	
130	135
140	
ggc tgc ata att tcc act gct agt tta agc tca act atg ggt ggt ggt	480
Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly	
145	150
155	160
tct tca cat gct tat tgt ggt tca aag cat gct gta tta ggc ctt act	528
Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr	
165	170
175	
agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt	576
Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys	
180	185
190	
ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg	624
Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Phe Thr Gly	
195	200
205	
att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat	672
Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn	
210	215
220	
ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt	720
Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu	
225	230
235	240
ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc	768
Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe	
245	250
255	
atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa	816
Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln	
260	265
270	
828	
tat cca gac tct	
Tyr Pro Asp Ser	
275	

&lt;210&gt; 10

&lt;211&gt; 276

&lt;212&gt; PRT

<213> *Forsythia x intermedia*

&lt;400&gt; 10

Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly

1

5

10

15

Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr

20

25

30

Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val

35

40

45

Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn

50

55

60

Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn  
 65 70 75 80

Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe  
 85 90 95

Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn  
 100 105 110

Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val  
 115 120 125

Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser  
 130 135 140

Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly  
 145 150 155 160

Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr  
 165 170 175

Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys  
 180 185 190

Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly  
 195 200 205

Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn  
 210 215 220

Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu  
 225 230 235 240

Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe  
 245 250 255

Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln  
 260 265 270

Tyr Pro Asp Ser  
 275

&lt;210&gt; 11

&lt;211&gt; 21

&lt;212&gt; PRT

<213> *Forsythia x intermedia*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(21)

<223> N-terminal peptide of *F. intermedia*  
secoisolariciresinol protein wherein Xaa at  
positions 3, 12 and 20 represents an unidentified  
amino acid residue

&lt;400&gt; 11

-14-

Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu  
1 5 10 15

Ile Thr Gly Xaa Ala  
20

<210> 12

<211> 17

<212> PRT

<213> *Forsythia x intermedia*

<400> 12

Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala  
1 5 10 15

Lys

<210> 13

<211> 15

<212> PRT

<213> *Forsythia x intermedia*

<400> 13

Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys  
1 5 10 15

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<220>

<221> misc\_feature

<222> (1)..(20)

<223> PCR primer wherein n at positions 3, 9, 15 and 18  
represents inosine

<400> 14

ggnathggng aracnacngc

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer wherein n at positions 3 and 9  
represents inosine

<400> 15  
ccngcrttng arAACATDAT

20

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer wherein n at positions 3 and 9  
represents inosine

<400> 16  
ccngcrttnc traACATDAT

20

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer

<400> 17  
attccgcttag attgcattga

20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature

<222> (1)..(20)  
<223> PCR primer wherein n at positions 3 and 9  
represent inosine

<400> 18  
ccngcrttnc traacatdat

20

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> T7 PCR primer

<400> 19  
aattaaacct cactaaaggg

20

<210> 20  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223> PCR primer

<400> 20  
cagttcgaa ctgcattcgc aag

23

<210> 21  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(22)  
<223> T7 PCR primer

<400> 21	22
cgggatatac ctcagcataa tg	
<210> 22	
<211> 816	
<212> DNA	
<213> <i>Forsythia x intermedia</i>	
<220>	
<221> CDS	
<222> (1)..(816)	
<400> 22	48
cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt	
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu	
1 5 10 15	
ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc	96
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe	
20 25 30	
tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta	144
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu	
35 40 45	
ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc	192
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile	
50 55 60	
cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac aac	240
His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn	
65 70 75 80	
aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca gga	288
Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly	
85 90 95	
att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca gac	336
Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp	
100 105 110	
ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc atg	384
Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met	
115 120 125	
aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata att	432
Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile	
130 135 140	
tcc act gct agt tta agc tca act atg ggt ggt tct tca cat gcc	480
Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His Ala	
145 150 155 160	
tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg gca	528
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala	
165 170 175	

gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct ttc 576  
 Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe  
 180 185 190

ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat gaa 624  
 Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu  
 195 200 205

gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt cca 672  
 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro  
 210 215 220

aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct agt 720  
 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Leu Tyr Leu Ala Ser  
 225 230 235 240

gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga ggg 768  
 Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly  
 245 250 255

ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat tct 816  
 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser  
 260 265 270

<210> 23

<211> 272

<212> PRT

<213> *Forsythia x intermedia*

<400> 23

Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu  
 1 5 10 15

Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe  
 20 25 30

Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu  
 35 40 45

Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile  
 50 55 60

His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn  
 65 70 75 80

Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly  
 85 90 95

Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp  
 100 105 110

Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met  
 115 120 125

Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile  
 130 135 140

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Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala  
145 150 155 160

Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala  
165 170 175

Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe  
180 185 190

Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu  
195 200 205

Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro  
210 215 220

Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser  
225 230 235 240

Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly  
245 250 255

Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser  
260 265 270

<210> 24  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(33)  
<223> PCR primer

<400> 24  
acatatgcag cttcgaaactg cattcgcaag aag

33

<210> 25  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(33)  
<223> PCR primer

<400> 25

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PCT/US99/08975

-20-

catatggca gacatgttac atgatcaatt gca

33